SEQUENCE LISTING

<110> Rosen, Craig A.
      Haseltine, William A.

<120> Albumin Fusion Proteins

<130> PF545

<140> Unassigned
<141> 2001-04-12

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<170> PatentIn Ver. 2.1

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Ile Ser Ala Asp Ala His Lys Ser
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gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag     96
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
                20                  25                  30

cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa     144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
            35                  40                  45

ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa     192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
        50                  55                  60

tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt     240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct     288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc     336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
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ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat     384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
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5

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gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga    432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
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aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg    480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                     150                 155                 160

tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc    528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                    165                 170                 175

tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg    576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
                180                 185                 190

tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa    624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
            195                 200                 205

aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc    672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
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aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa    720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225                 230                 235                 240

gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac    768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc    816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac    864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
            275                 280                 285

tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca    912
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct    960
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga   1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca   1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
                340                 345                 350

tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa   1104
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
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6

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tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct   1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
        370                    375                    380

cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag   1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                    390                    395                    400

tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc   1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                    410                    415

caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa   1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
                420                    425                    430

gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt   1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
                435                    440                    445

gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat   1392
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
        450                    455                    460

gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc   1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                    470                    475                    480

ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca   1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                    490                    495

tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat   1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
                500                    505                    510

ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca   1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                    520                    525

ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg   1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
        530                    535                    540

aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag   1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                    550                    555                    560

gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt   1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                    570                    575

gct gca agt caa gct gcc tta ggc tta taacatctac atttaaaagc atctcag 1782
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Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
            35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
        50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
                100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
            115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
        130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
            195                 200                 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210                 215                 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225                 230                 235                 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
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Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
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Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
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Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340             345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355             360             365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370             375             380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385             390             395                     400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
            405             410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420             425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435             440             445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450             455             460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465             470             475                     480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
            485             490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500             505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515             520             525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530             535             540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
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Ala Ala Ser Gln Ala Ala Leu Gly Leu
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12

of the Therapeutic Protein

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protein in which the albumin  moiety is c-terminal of the
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the Therapeutic Protein

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<222> (49)
<223> n equals a,t,g, or c
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16

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<220>
<221> misc feature
<222> (50)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (51)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (52)
<223> n equals a,t,g, or c

<400> 28
ctttaaatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnn nn          52


<210> 29
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> signal peptide of natural human serum albumin protein

<400> 29
Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
 1               5               10               15

Tyr Ser Arg Ser Leu Asp Lys Arg
              20

<210> 30
<211> 114
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of PC4:HSA
albumin fusion VECTOR

<220>
<221> misc_feature
<222> (5)..(10)
<223> BamHI retsriction site

<220>
<221> misc_feature
<222> (11)..(16)
<223> Hind III retsriction site

<220>
<221> misc_feature
<222> (17)..(27)
<223> Kozak sequence
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<220>
<221> misc_feature
<222> (25)..(97)
<223> cds natural signal sequence of human serum albumin

<220>
<221> misc_feature
<222> (75)..(81)
<223> XhoI restriction site

<220>
<221> misc_feature
<222> (98)..(114)
<223> cds first six amino acids of human serum albumin

<400> 30
tcagggatcc aagcttccgc caccatgaag tgggtaacct ttatttccct tctttttctc 60

tttagctcgg cttactcgag gggtgtgttt cgtcgagatg cacacaagag tgag   114

<210> 31
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for generation of
PC4:HSA albumin fusion VECTOR

<220>
<221> misc_feature
<222> (6)..(11)
<223> Asp718 restriction site

<220>
<221> misc_feature
<222> (12)..(17)
<223> EcoRI restriction site

<220>
<221> misc_feature
<222> (15)..(17)
<223> reverse complement of stop codon

<220>
<221> misc_feature
<222> (18)..(25)
<223> AscI restriction site

<220>
<221> misc_feature
<222> (18)..(43)
<223> reverse complement of DNA sequence encoding last 9 amino acids

<400> 31
gcagcggtac cgaattcggc gcgccttata agcctaaggc agc   43

18

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for inserting Therapeutic
protein into pC4:HSA vector

<220>
<221> misc feature
<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (31)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (32)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (33)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (34)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (35)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (36)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (37)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c

19

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<220>
<221> misc feature
<222> (39)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (41)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (44)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<400> 32
ccgccgctcg aggggtgtgt ttcgtcgann nnnnnnnnnn nnnnnn                          46

<210> 33
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for inserting Therapeutic
protein into pC4:HSA vector

<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c

<220>
<221> misc feature
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20

<222> (39)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (41)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (44)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (47)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (48)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (49)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (50)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (51)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (52)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (53)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (54)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<400> 33
agtcccatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnn nnnnn   55

<210> 34
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Stanniocalcin signal peptide

<400> 34
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Leu Val Ile Ser Ala Ser
  1   5   10   15

Ala

<210> 35
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Synthetic signal peptide

<400> 35
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu
  1   5   10   15

Trp Ala Pro Ala Arg Gly
              20

<210> 36
<211> 23
<212> DNA

22

<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 36
caggtgcagc tggtgcagtc tgg   23

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 37
caggtcaact taagggagtc tgg   23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 38
gaggtgcagc tggtggagtc tgg   23

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 39
caggtgcagc tgcaggagtc ggg   23

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 40
gaggtgcagc tgttgcagtc tgc

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 41
caggtacagc tgcagcagtc agg

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 42
tgaggagacg gtgaccaggg tgcc

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 43
tgaagagacg gtgaccattg tccc

<210> 44
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 44
tgaggagacg gtgaccaggg ttcc

<210> 45
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 45
tgaggagacg gtgaccgtgg tccc   24

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 46
gacatccaga tgacccagtc tcc   23

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 47
gatgttgtga tgactcagtc tcc   23

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 48
gatattgtga tgactcagtc tcc   23

<210> 49
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 49

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gaaattgtgt tgacgcagtc tcc                                    23


<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 50
gacatcgtga tgacccagtc tcc                                    23


<210> 51
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 51
gaaacgacac tcacgcagtc tcc                                    23


<210> 52
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 52
gaaattgtgc tgactcagtc tcc                                    23


<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 53
cagtctgtgt tgacgcagcc gcc                                    23


<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<221>primer_bind
<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 54
cagtctgccc tgactcagcc tgc   23

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 55
tcctatgtgc tgactcagcc acc   23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 56
tcttctgagc tgactcagga ccc   23

<210> 57
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 57
cacgttatac tgactcaacc gcc   23

<210> 58
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 58
caggctgtgc tcactcagcc gtc   23

<210> 59

27

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<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 59
aattttatgc tgactcagcc cca                                    23

<210> 60
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for
amplifying human VL domains

<400> 60
acgtttgatt tccaccttgg tccc                                   24

<210> 61
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for
amplifying human VL domains

<400> 61
acgtttgatc tccagcttgg tccc                                   24

<210> 62
<211> 24·
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for
amplifying human VL domains

<400> 62
acgtttgata tccactttgg tccc                                   24

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for
amplifying human VL domains
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<400> 63
acgtttgatc tccaccttgg tccc                          24

<210> 64
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for
amplifying human VL domains

<400> 64
acgtttaatc tccagtcgtg tccc                          24

<210> 65
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 65
cagtctgtgt tgacgcagcc gcc                           23

<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 66
cagtctgccc tgactcagcc tgc                           23

<210> 67
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 67
tcctatgtgc tgactcagcc acc                           23

<210> 68
<211> 23
<212> DNA
<213> Artificial Sequence
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<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 68
tcttctgagc tgactcagga ccc                                          23


<210> 69
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 69
cacgttatac tgactcaacc gcc                                          23


<210> 70
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 70
caggctgtgc tcactcagcc gtc                                          23


<210> 71
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 71
aattttatgc tgactcagcc cca                                          23


<210> 72
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221>turn
<223>Linker peptide that may be used to join VH
and VL domains in an scFv.

<400> 72
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
```

30

<210> 73
<211> 23
<212> PRT
<213> Homo sapiens

<400> 73
Cys Cys Cys Ala Ala Gly Ala Ala Thr Thr Cys Cys Cys Thr Thr Ala
1   5   10   15

Thr Cys Cys Ala Gly Gly Cys
                20

<210> 74
<211> 429
<212> PRT
<213> Homo sapiens

<400> 74
Met Cys Pro Gly Ala Leu Trp Val Ala Leu Pro Leu Leu Ser Leu Leu
1   5   10   15

Ala Gly Ser Leu Gln Gly Lys Pro Leu Gln Ser Trp Gly Arg Gly Ser
            20   25   30

Ala Gly Gly Asn Ala His Ser Pro Leu Gly Val Pro Gly Gly Gly Leu
            35   40   45

Pro Glu His Thr Phe Asn Leu Lys Met Phe Leu Glu Asn Val Lys Val
        50   55   60

Asp Phe Leu Arg Ser Leu Asn Leu Ser Gly Val Pro Ser Gln Asp Lys
    65   70   75   80

Thr Arg Val Glu Pro Pro Gln Tyr Met Ile Asp Leu Tyr Asn Arg Tyr
                85   90   95

Thr Ser Asp Lys Ser Thr Thr Pro Ala Ser Asn Ile Val Arg Ser Phe
                100   105   110

Ser Met Glu Asp Ala Ile Ser Ile Thr Ala Thr Glu Asp Phe Pro Phe
            115   120   125

Gln Lys His Ile Leu Leu Phe Asn Ile Ser Ile Pro Arg His Glu Gln
            130   135   140

Ile Thr Arg Ala Glu Leu Arg Leu Tyr Val Ser Cys Gln Asn His Val
145   150   155   160

Asp Pro Ser His Asp Leu Lys Gly Ser Val Val Ile Tyr Asp Val Leu
                165   170   175

Asp Gly Thr Asp Ala Trp Asp Ser Ala Thr Glu Thr Lys Thr Phe Leu
            180   185   190

Val Ser Gln Asp Ile Gln Asp Glu Gly Trp Glu Thr Leu Glu Val Ser
            195   200   205

Ser Ala Val Lys Arg Trp Val Arg Ser Asp Ser Thr Lys Ser Lys Asn

31

```
Lys Leu Glu Val Thr Val Glu Ser His Arg Lys Gly Cys Asp Thr Leu
225                230                235                240

Asp Ile Ser Val Pro Pro Gly Ser Arg Asn Leu Pro Phe Phe Val Val
                245                250                255

Phe Ser Asn Asp His Ser Ser Gly Thr Lys Glu Thr Arg Leu Glu Leu
                260                265                270

Arg Glu Met Ile Ser His Glu Gln Glu Ser Val Leu Lys Lys Leu Ser
                275                280                285

Lys Asp Gly Ser Thr Glu Ala Gly Glu Ser Ser His Glu Glu Asp Thr
                290                295                300

Asp Gly His Val Ala Ala Gly Ser Thr Leu Ala Arg Arg Lys Arg Ser
305                310                315                320

Ala Gly Ala Gly Ser His Cys Gln Lys Thr Ser Leu Arg Val Asn Phe
                325                330                335

Glu Asp Ile Gly Trp Asp Ser Trp Ile Ile Ala Pro Lys Glu Tyr Glu
                340                345                350

Ala Tyr Glu Cys Lys Gly Gly Cys Phe Phe Pro Leu Ala Asp Asp Val
                355                360                365

Thr Pro Thr Lys His Ala Ile Val Gln Thr Leu Val His Leu Lys Phe
                370                375                380

Pro Thr Lys Val Gly Lys Ala Cys Cys Val Pro Thr Lys Leu Ser Pro
385                390                395                400

Ile Ser Val Leu Tyr Lys Asp Asp Met Gly Val Pro Thr Leu Lys Tyr
                405                410                415

His Tyr Glu Gly Met Ser Val Ala Glu Cys Gly Cys Arg
                420                425
```

<210> 75
<211> 280
<212> PRT
<213> Homo sapiens

<400> 75

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Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val Leu
1               5                10                15

Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn Val Arg
                20                25                30

Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly Asp Trp Met
                35                40                45

Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln Asn Leu Gln Pro
                50                55                60

Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp Leu Glu Val Asn Ile
```

Ala Lys Val Asp Val Thr Glu Gln Pro Gly Leu Ser Gly Arg Phe Ile
                    85   90   95

Ile Thr Ala Leu Pro Thr Ile Tyr His Cys Lys Asp Gly Glu Phe Arg
                100   105   110

Arg Tyr Gln Gly Pro Arg Thr Lys Lys Asp Phe Ile Asn Phe Ile Ser
        115   120   125

Asp Lys Glu Trp Lys Ser Ile Glu Pro Val Ser Ser Trp Phe Gly Pro
    130   135   140

Gly Ser Val Leu Met Ser Ser Met Ser Ala Leu Phe Gln Leu Ser Met
145   150   155   160

Trp Ile Arg Thr Cys His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro
                165   170   175

Val Trp Gly Ser Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly
            180   185   190

Leu Leu Leu Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro
        195   200   205

Ser Lys Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu
    210   215   220

Leu Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
225   230   235   240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu Gly
                245   250   255

Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser Leu Gly
            260   265   270

Pro Ser Leu Ala Thr Asp Lys Ser
        275   280

<210> 76
<211> 112
<212> PRT
<213> Homo sapiens

<400> 76
Met Phe Trp Val Met Glu Thr Ala Lys Pro Pro Val Ser Glu Asp Ser
1   5   10   15

Phe Arg Leu Pro Arg Lys Trp Gly Trp Arg Thr Glu Ala Thr Ala Pro
                20   25   30

His Ala Pro Val Pro Gln Ser Ile Cys Pro Arg Tyr Thr Ser Pro Cys
            35   40   45

Ala Pro His Asp Cys Gly Ser Gln Thr Val Gln Gly Asn Ser Leu Ser
        50   55   60

Leu Phe Tyr Thr Leu Ser His Lys Ala Pro Gln Leu Pro His Arg Val

33

Pro Ala Pro Leu Phe Cys Lys Tyr Val Lys Arg Lys Lys Cys Lys Arg
                    85   90   95

Trp Ser Leu Gly Trp Ser Ser Ser Leu Gln Leu Arg Leu Leu Thr Met
                100   105   110

<210> 77
<211> 346
<212> PRT
<213> Homo sapiens

<400> 77
Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr Ala
  1   5   10   15

Gly Trp Leu Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala Leu Glu
                 20   25   30

Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser Pro Asn Lys
            35   40   45

Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val Cys Thr Glu Ala
       50   55   60

Val Gly Ala Val Glu Thr Ile His Gly Gln Phe Ser Leu Ala Val Arg
 65   70   75   80

Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn Asp Arg Gly Leu Asp Leu
                85   90   95

His Gly Leu Leu Ala Phe Ile Gln Leu Gln Gln Cys Ala Gln Asp Arg
                100   105   110

Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg Ala Leu Asp Pro Ala Gly
       115   120   125

Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val Glu Cys Tyr Ser Cys Val
       130   135   140

Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr Ser Pro Pro Val Val Ser
145   150   155   160

Cys Tyr Asn Ala Ser Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn
                165   170   175

Val Thr Leu Thr Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly
                180   185   190

Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly
            195   200   205

Phe Thr Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp
       210   215   220

Leu Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg
225   230   235   240

Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val Thr

```
                245                      250                      255
Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys Pro Met
            260                  265                  270

Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala
            275                  280                  285

Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln
    290                  295                  300

Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln
305                  310                  315                  320

Pro His Asn Lys Gly Cys Val Ala Pro Thr Ala Gly Leu Ala Ala Leu
            325                  330                  335

Leu Leu Ala Val Ala Ala Gly Val Leu Leu
            340                  345
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<210> 78
<211> 272
<212> PRT
<213> Homo sapiens

<400> 78
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Met Lys Gly Lys Lys Gly Ile Val Ala Ala Ser Gly Ser Glu Thr Glu
 1               5                  10                  15

Asp Glu Asp Ser Met Asp Ile Pro Leu Asp Leu Ser Ser Ser Ala Gly
            20                  25                  30

Ser Gly Lys Arg Arg Arg Arg Gly Asn Leu Pro Lys Glu Ser Val Gln
            35                  40                  45

Ile Leu Arg Asp Trp Leu Tyr Glu His Arg Tyr Asn Ala Tyr Pro Ser
    50                  55                  60

Glu Gln Glu Lys Ala Leu Leu Ser Gln Gln Thr His Leu Ser Thr Leu
65                  70                  75                  80

Gln Val Cys Asn Trp Phe Ile Asn Ala Arg Arg Arg Leu Leu Pro Asp
                85                  90                  95

Met Leu Arg Lys Asp Gly Lys Asp Pro Asn Gln Phe Thr Ile Ser Arg
            100                 105                 110

Arg Gly Ala Lys Ile Ser Glu Thr Ser Ser Val Glu Ser Val Met Gly
            115                 120                 125

Ile Lys Asn Phe Met Pro Ala Leu Glu Glu Thr Pro Phe His Ser Cys
            130                 135                 140

Thr Ala Gly Pro Asn Pro Thr Leu Gly Arg Pro Leu Ser Pro Lys Pro
145                 150                 155                 160

Ser Ser Pro Gly Ser Val Leu Ala Arg Pro Ser Val Ile Cys His Thr
            165                 170                 175

Thr Val Thr Ala Leu Lys Asp Val Pro Phe Ser Leu Cys Gln Ser Val
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35

Gly Val Gly Gln Asn Thr Asp Ile Gln Gln Ile Ala Ala Lys Asn Phe
        195   200   205

Thr Asp Thr Ser Leu Met Tyr Pro Glu Asp Thr Cys Lys Ser Gly Pro
    210   215   220

Ser Thr Asn Thr Gln Ser Gly Leu Phe Asn Thr Pro Pro Pro Thr Pro
225   230   235   240

Pro Asp Leu Asn Gln Asp Phe Ser Gly Phe Gln Leu Leu Val Asp Val
            245   250   255

Ala Leu Lys Arg Ala Ala Glu Met Glu Leu Gln Ala Lys Leu Thr Ala
        260   265   270

<210> 79
<211> 167
<212> PRT
<213> Homo sapiens

<400> 79
Met Leu Thr Val Ala Leu Leu Ala Leu Leu Cys Ala Ser Ala Ser Gly
  1   5   10   15

Asn Ala Ile Gln Ala Arg Ser Ser Ser Tyr Ser Gly Glu Tyr Gly Gly
            20   25   30

Gly Gly Gly Lys Arg Phe Ser His Ser Gly Asn Gln Leu Asp Gly Pro
            35   40   45

Ile Thr Ala Leu Arg Val Arg Val Asn Thr Tyr Tyr Ile Val Gly Leu
      50   55   60

Gln Val Arg Tyr Gly Lys Val Trp Ser Asp Tyr Val Gly Gly Arg Asn
65   70   75   80

Gly Asp Leu Glu Glu Ile Phe Leu His Pro Gly Glu Ser Val Ile Gln
                85   90   95

Val Ser Gly Lys Tyr Lys Trp Tyr Leu Lys Lys Leu Val Phe Val Thr
            100   105   110

Asp Lys Gly Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe
            115   120   125

Asn Ala Val Pro Leu His Pro Asn Thr Val Leu Arg Phe Ile Ser Gly
            130   135   140

Arg Ser Gly Ser Leu Ile Asp Ala Ile Gly Leu His Trp Asp Val Tyr
145   150   155   160

Pro Thr Ser Cys Ser Arg Cys
                165

36